

SEQUENCE LISTING

Sub
a1
<110> KIKKOMAN CORPORATION

<120> LUCIFERASE AND A METHOD FOR DETECTING INTRACELLULAR ATP
USING THE SAME

<130> P98-0634

<140>

<141>

<150> JP97/361022

<151> 1997-12-26

<160> 6

<170> PatentIn Ver. 2.0

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Synthetic DNA

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tgttgtactt aagaaaggaa aat

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<400> 2

23

acagctcccg gaagctcacc agc

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<211> 1644

<212> DNA

<213> *Luciola lateralis*

<220>

<221> CDS

<222> (1)..(1644)

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Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Tyr Gly Pro Glu Pro

1

5

10

15

ttt tac cct att gaa gag gga tct gct gga gca caa ttg cgc aag tat 96
Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr

20

25

30

atg gat cga tat gca aaa ctt gga gca att gct ttt act aac gca ctt 144
Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu

35

40

45

acc ggt gtc gat tat acg tac gcc gaa tac tta gaa aaa tca tgc tgt 192
Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys

50

55

60

cta gga gag gct tta aag aat tat ggt ttg gtt gtt gat gga aga att 240
Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile

65

70

75

80

gcg tta tgc agt gaa aac tgt gaa gaa ttc ttt att cct gta tta gcc 288
Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Leu Ala

85

90

95

ggt tta ttt ata ggt gtc ggt gtg gct cca act aat gag att tac act 336
Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr

100

105

110

cta cgt gaa ttg gtt cac agt tta ggc atc tct aag cca aca att gta 384
Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val

115

120

125

ttt agt tct aaa aaa gga tta gat aaa gtt ata act gta caa aaa acg 432
Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr

130

135

140

gta act gct att aaa acc att gtt ata ttg gac agc aaa gtg gat tat 480
Val Thr Ala Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr

145

150

155

160

aga ggt tat caa tcc atg gac aac ttt att aaa aaa aac act cca caa 528
Arg Gly Tyr Gln Ser Met Asp Asn Phe Ile Lys Lys Asn Thr Pro Gln

165

170

175

ggt ttc aaa gga tca agt ttt aaa act gta gaa gtt aac cgc aaa gaa 576
Gly Phe Lys Gly Ser Ser Phe Lys Thr Val Glu Val Asn Arg Lys Glu

180

185

190

caa gtt gct ctt ata atg aac tct tcg ggt tca acc ggt ttg cca aaa 624
Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys

195

200

205

ggt gtg caa ctt act cat gaa aat ttg gtc act aga ttt tct cac gct 672
Gly Val Gln Leu Thr His Glu Asn Leu Val Thr Arg Phe Ser His Ala

210

215

220

aga gat cca att tat gga aac caa gtt tca cca ggc acg gct att tta 720
Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Ile Leu

225

230

235

240

act gta gta cca ttc cat cat ggt ttt ggt atg ttt act act tta ggc 768

Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly
 245 250 255

tat cta act tgt ggt ttt cgt att gtc atg tta acg aaa ttt gac gaa 816
 Tyr Leu Thr Cys Gly Phe Arg Ile Val Met Leu Thr Lys Phe Asp Glu
 260 265 270

gag act ttt tta aaa aca ctg caa gat tac aaa tgt tca agc gtt att 864
 Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Ser Ser Val Ile
 275 280 285

ctt gta ccg act ttg ttt gca att ctt aat aga agt gaa tta ctc gat 912
 Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Arg Ser Glu Leu Leu Asp
 290 295 300

aaa tat gat tta tca aat tta gtt gaa att gca tct ggc gga gca cct 960
 Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro
 305 310 315 320

tta tct aaa gaa att ggt gaa gct gtt gct aga cgt ttt aat tta ccg 1008
 Leu Ser Lys Glu Ile Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro
 325 330 335

ggt gtt cgt caa ggc tat ggt tta aca gaa aca acc tct gca att att 1056
 Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile
 340 345 350

atc aca ccg gaa ggc gat gat aaa cca ggt gct tct ggc aaa gtt gtg 1104
 Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val

355

360

365

cca tta ttt aaa gca aaa gtt atc gat ctt gat act aaa aaa act ttg 1152
 Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Thr Leu
 370 375 380

ggc ccg aac aga cgt gga gaa gtt tgt gta aag ggt cct atg ctt atg 1200
 Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met
 385 390 395 400

aaa ggt tat gta gat aat cca gaa gca aca aga gaa atc ata gat gaa 1248
 Lys Gly Tyr Val Asp Asn Pro Glu Ala Thr Arg Glu Ile Ile Asp Glu
 405 410 415

gaa ggt tgg ttg cac aca gga gat att ggg tat tac gat gaa gaa aaa 1296
 Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys
 420 425 430

cat ttc ttt atc gtg gat cgt ttg aag tct tta atc aaa tac aaa gga 1344
 His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly
 435 440 445

tat caa gta cca cct gct gaa tta gaa tct gtt ctt ttg caa cat cca 1392
 Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro
 450 455 460

aat att ttt gat gcc gcc gtt gct gcc gtt cca gat cct ata gct ggt 1440
 Asn Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Ile Ala Gly
 465 470 475 480

gag ctt ccg gga gct gtt gtt gta ctt aag aaa gga aaa tct atg act 1488
 Glu Leu Pro Gly Ala Val Val Val Leu Lys Lys Gly Lys Ser Met Thr

485

490

495

gaa aaa gaa gta atg gat tac gtt gct agt caa gtt tca aat gca aaa 1536
 Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys

500

505

510

cgt ttg cgt ggt ggt gtc cgt ttt gtg gac gaa gta cct aaa ggt ctc 1584
 Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu

515

520

525

act ggt aaa att gac ggt aaa gca att aga gaa ata ctg aag aaa cca 1632
 Thr Gly Lys Ile Asp Gly Lys Ala Ile Arg Glu Ile Leu Lys Lys Pro

530

535

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gtt gct aag atg
 Val Ala Lys Met

1644

545

<210> 4

<211> 548

<212> PRT

<213> *Luciola lateralis*

<400> 4

Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Tyr Gly Pro Glu Pro

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Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr
20 25 30

Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu
35 40 45

Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys
50 55 60

Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile
65 70 75 80

Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Leu Ala
85 90 95

Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr
100 105 110

Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val
115 120 125

Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr
130 135 140

Val Thr Ala Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr
145 150 155 160

Arg Gly Tyr Gln Ser Met Asp Asn Phe Ile Lys Lys Asn Thr Pro Gln

165

170

175

Gly Phe Lys Gly Ser Ser Phe Lys Thr Val Glu Val Asn Arg Lys Glu

180

185

190

Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys

195

200

205

Gly Val Gln Leu Thr His Glu Asn Leu Val Thr Arg Phe Ser His Ala

210

215

220

Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Ile Leu

225

230

235

240

Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly

245

250

255

Tyr Leu Thr Cys Gly Phe Arg Ile Val Met Leu Thr Lys Phe Asp Glu

260

265

270

Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Ser Ser Val Ile

275

280

285

Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Arg Ser Glu Leu Leu Asp

290

295

300

Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro

305

310

315

320

Leu Ser Lys Glu Ile Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro
325 330 335

Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile
340 345 350

Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val
355 360 365

Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Thr Leu
370 375 380

Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met
385 390 395 400

Lys Gly Tyr Val Asp Asn Pro Glu Ala Thr Arg Glu Ile Ile Asp Glu
405 410 415

Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys
420 425 430

His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly
435 440 445

Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro
450 455 460

Asn Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Ile Ala Gly
465 470 475 480

Glu Leu Pro Gly Ala Val Val Val Leu Lys Lys Gly Lys Ser Met Thr
 485 490 495

Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys
 500 505 510

Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu
 515 520 525

Thr Gly Lys Ile Asp Gly Lys Ala Ile Arg Glu Ile Leu Lys Lys Pro
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Val Ala Lys Met
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<210> 5

<211> 1644

<212> DNA

<213> *Luciola lateralis*

<220>

<221> CDS

<222> (1)..(1644)

<400> 5

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 Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Tyr Gly Pro Glu Pro

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15

ttt tac cct att gaa gag gga tct gct gga gca caa ttg cgc aag tat 96

Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr

20

25

30

atg gat cga tat gca aaa ctt gga gca att gct ttt act aac gca ctt 144

Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu

35

40

45

acc ggt gtc gat tat acg tac gcc gaa tac tta gaa aaa tca tgc tgt 192

Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys

50

55

60

cta gga gag gct tta aag aat tat ggt ttg gtt gtt gat gga aga att 240

Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile

65

70

75

80

gcg tta tgc agt gaa aac tgt gaa gaa ttc ttt att cct gta tta gcc 288

Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Leu Ala

85

90

95

ggt tta ttt ata ggt gtc ggt gtg gct cca act aat gag att tac act 336

Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr

100

105

110

cta cgt gaa ttg gtt cac agt tta ggc atc tct aag cca aca att gta 384

Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val

115

120

125

ttt agt tct aaa aaa gga tta gat aaa gtt ata act gta caa aaa acg 432
Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr

130

135

140

gta act gct att aaa acc att gtt ata ttg gac agc aaa gtg gat tat 480
Val Thr Ala Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr

145

150

155

160

aga ggt tat caa tcc atg gac aac ttt att aaa aaa aac act cca caa 528
Arg Gly Tyr Gln Ser Met Asp Asn Phe Ile Lys Lys Asn Thr Pro Gln

165

170

175

ggt ttc aaa gga tca agt ttt aaa act gta gaa gtt aac cgc aaa gaa 576
Gly Phe Lys Gly Ser Ser Phe Lys Thr Val Glu Val Asn Arg Lys Glu

180

185

190

caa gtt gct ctt ata atg aac tct tcg ggt tca acc ggt ttg cca aaa 624
Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys

195

200

205

ggt gtg caa ctt act cat gaa aat atc gtc act aga ttt tct cac gct 672
Gly Val Gln Leu Thr His Glu Asn Ile Val Thr Arg Phe Ser His Ala

210

215

220

aga gat cca att tat gga aac caa gtt tca cca ggc acg gct att tta 720
Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Ile Leu

225

230

235

240

act gta gta cca ttc cat cat ggt ttt ggt atg ttt act act tta ggc 768
 Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly

245

250

255

tat cta act tgt ggt ttt cgt att gtc atg tta acg aaa ttt gac gaa 816
 Tyr Leu Thr Cys Gly Phe Arg Ile Val Met Leu Thr Lys Phe Asp Glu

260

265

270

gag act ttt tta aaa aca ctg caa gat tac aaa tgt tca agc gtt att 864
 Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Ser Ser Val Ile

275

280

285

ctt gta ccg act ttg ttt gca att ctt aat aga agt gaa tta ctc gat 912
 Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Arg Ser Glu Leu Leu Asp

290

295

300

aaa tat gat tta tca aat tta gtt gaa att gca tct ggc gga gca cct 960
 Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro

305

310

315

320

tta tct aaa gaa att ggt gaa gct gtt gct aga cgt ttt aat tta ccg 1008
 Leu Ser Lys Glu Ile Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro

325

330

335

ggt gtt cgt caa ggc tat ggt tta aca gaa aca acc tct gca att att 1056
 Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile

340

345

350

atc aca ccg gaa ggc gat gat aaa cca ggt gct tct ggc aaa gtt gtg 1104

Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val
 355 360 365

cca tta ttt aaa gca aaa gtt atc gat ctt gat act aaa aaa act ttg 1152
 Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Thr Leu
 370 375 380

ggc ccg aac aga cgt gga gaa gtt tgt gta aag ggt cct atg ctt atg 1200
 Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met
 385 390 395 400

aaa ggt tat gta gat aat cca gaa gca aca aga gaa atc ata gat gaa 1248
 Lys Gly Tyr Val Asp Asn Pro Glu Ala Thr Arg Glu Ile Ile Asp Glu
 405 410 415

gaa ggt tgg ttg cac aca gga gat att ggg tat tac gat gaa gaa aaa 1296
 Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys
 420 425 430

cat ttc ttt atc gtg gat cgt ttg aag tct tta atc aaa tac aaa gga 1344
 His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly
 435 440 445

tat caa gta cca cct gct gaa tta gaa tct gtt ctt ttg caa cat cca 1392
 Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro
 450 455 460

aat att ttt gat gcc ggc gtt gct ggc gtt cca gat cct ata gct ggt 1440
 Asn Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Ile Ala Gly

465

470

475

480

gag ctt ccg gga gct gtt gtt gta ctt aag aaa gga aaa tct atg act 1488
 Glu Leu Pro Gly Ala Val Val Val Leu Lys Lys Gly Lys Ser Met Thr

485

490

495

gaa aaa gaa gta atg gat tac gtt gct agt caa gtt tca aat gca aaa 1536
 Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys

500

505

510

cgt ttg cgt ggt ggt gtc cgt ttt gtg gac gaa gta cct aaa ggt ctc 1584
 Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu

515

520

525

act ggt aaa att gac ggt aaa gca att aga gaa ata ctg aag aaa cca 1632
 Thr Gly Lys Ile Asp Gly Lys Ala Ile Arg Glu Ile Leu Lys Lys Pro

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gtt gct aag atg

1644

Val Ala Lys Met

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<210> 6

<211> 548

<212> PRT

<213> *Luciola lateralis*

<400> 6

Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Tyr Gly Pro Glu Pro
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Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Ala Gln Leu Arg Lys Tyr
20 25 30

Met Asp Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr Asn Ala Leu
35 40 45

Thr Gly Val Asp Tyr Thr Tyr Ala Glu Tyr Leu Glu Lys Ser Cys Cys
50 55 60

Leu Gly Glu Ala Leu Lys Asn Tyr Gly Leu Val Val Asp Gly Arg Ile
65 70 75 80

Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe Phe Ile Pro Val Leu Ala
85 90 95

Gly Leu Phe Ile Gly Val Gly Val Ala Pro Thr Asn Glu Ile Tyr Thr
100 105 110

Leu Arg Glu Leu Val His Ser Leu Gly Ile Ser Lys Pro Thr Ile Val
115 120 125

Phe Ser Ser Lys Lys Gly Leu Asp Lys Val Ile Thr Val Gln Lys Thr
130 135 140

Val Thr Ala Ile Lys Thr Ile Val Ile Leu Asp Ser Lys Val Asp Tyr
145 150 155 160

Arg Gly Tyr Gln Ser Met Asp Asn Phe Ile Lys Lys Asn Thr Pro Gln
165 170 175

Gly Phe Lys Gly Ser Ser Phe Lys Thr Val Glu Val Asn Arg Lys Glu
180 185 190

Gln Val Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys
195 200 205

Gly Val Gln Leu Thr His Glu Asn Ile Val Thr Arg Phe Ser His Ala
210 215 220

Arg Asp Pro Ile Tyr Gly Asn Gln Val Ser Pro Gly Thr Ala Ile Leu
225 230 235 240

Thr Val Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly
245 250 255

Tyr Leu Thr Cys Gly Phe Arg Ile Val Met Leu Thr Lys Phe Asp Glu
260 265 270

Glu Thr Phe Leu Lys Thr Leu Gln Asp Tyr Lys Cys Ser Ser Val Ile
275 280 285

Leu Val Pro Thr Leu Phe Ala Ile Leu Asn Arg Ser Glu Leu Leu Asp
290 295 300

Lys Tyr Asp Leu Ser Asn Leu Val Glu Ile Ala Ser Gly Gly Ala Pro

305

310

315

320

Leu Ser Lys Glu Ile Gly Glu Ala Val Ala Arg Arg Phe Asn Leu Pro

325

330

335

Gly Val Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Ile

340

345

350

Ile Thr Pro Glu Gly Asp Asp Lys Pro Gly Ala Ser Gly Lys Val Val

355

360

365

Pro Leu Phe Lys Ala Lys Val Ile Asp Leu Asp Thr Lys Lys Thr Leu

370

375

380

Gly Pro Asn Arg Arg Gly Glu Val Cys Val Lys Gly Pro Met Leu Met

385

390

395

400

Lys Gly Tyr Val Asp Asn Pro Glu Ala Thr Arg Glu Ile Ile Asp Glu

405

410

415

Glu Gly Trp Leu His Thr Gly Asp Ile Gly Tyr Tyr Asp Glu Glu Lys

420

425

430

His Phe Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly

435

440

445

Tyr Gln Val Pro Pro Ala Glu Leu Glu Ser Val Leu Leu Gln His Pro

450

455

460

Asn Ile Phe Asp Ala Gly Val Ala Gly Val Pro Asp Pro Ile Ala Gly
465 470 475 480

Glu Leu Pro Gly Ala Val Val Val Leu Lys Lys Gly Lys Ser Met Thr
485 490 495

Glu Lys Glu Val Met Asp Tyr Val Ala Ser Gln Val Ser Asn Ala Lys
500 505 510

Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu
515 520 525

Thr Gly Lys Ile Asp Gly Lys Ala Ile Arg Glu Ile Leu Lys Lys Pro
530 535 540

Val Ala Lys Met
545